

SEQUENCE LISTING

<110> Alitalo, et al.

<120> VEGF-B AND PDGF MODULATION OF STEM CELLS

<130> 28967/39140B

<140> To be assigned

<141> Herewith

<150> US 60/445,021

<151> 2003-02-04

<150> US 60/471,412

<151> 2003-05-16

<160> 30

<170> PatentIn version 3.2

<210> 1

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<212> DNA

<213> Homo sapiens

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Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
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Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
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Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
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Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
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Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro Arg
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Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys Arg
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Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
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Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
 30 35 40

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
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Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
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Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
 80 85 90

Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
 95 100 105

Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg
 110 115 120

Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro
 125 130 135

Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser Ala
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His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala Ala
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Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala
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aacttgtgtc rtgctgatag gacagactgg atttttcata tttcttatta aaatttctgc     1680
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35 40 45

Ile Ile Thr Val Ser Thr Asn Gly Ser Ile His Ser Pro Arg Phe Pro
50 55 60

His Thr Tyr Pro Arg Asn Thr Val Leu Val Trp Arg Leu Val Ala Val
65 70 75 80

Glu Glu Asn Val Trp Ile Gln Leu Thr Phe Asp Glu Arg Phe Gly Leu
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Glu Asp Pro Glu Asp Asp Ile Cys Lys Tyr Asp Phe Val Glu Val Glu
100 105 110

Glu Pro Ser Asp Gly Thr Ile Leu Gly Arg Trp Cys Gly Ser Gly Thr
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Val Pro Gly Lys Gln Ile Ser Lys Gly Asn Gln Ile Arg Ile Arg Phe
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Val Ser Asp Glu Tyr Phe Pro Ser Glu Pro Gly Phe Cys Ile His Tyr
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Asn Ile Val Met Pro Gln Phe Thr Glu Ala Val Ser Pro Ser Val Leu
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Pro Pro Ser Ala Leu Pro Leu Asp Leu Leu Asn Asn Ala Ile Thr Ala
180 185 190

Phe Ser Thr Leu Glu Asp Leu Ile Arg Tyr Leu Glu Pro Glu Arg Trp
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Gln Leu Asp Leu Glu Asp Leu Tyr Arg Pro Thr Trp Gln Leu Leu Gly
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Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile Phe Trp Pro
260 265 270

Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala Cys Cys Leu
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His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser Lys Val Thr Lys Lys
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Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr Gly Val Arg Gly Leu
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 <213> Homo sapiens

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 35 40 45

Leu Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val
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Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr
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Trp Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp
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Asn Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp
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Phe Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly
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Arg Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr
 130 135 140

Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys
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Pro Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala
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Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly
 180 185 190

Val Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp
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Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu
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Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr
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Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser
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Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys
 260 265 270

Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala
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Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly
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Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser
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Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly
 325 330 335

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Pro Arg
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 35 40 45

Lys Arg Cys Gly Gly Asn Cys Ala Cys Cys Leu His Asn Cys Asn Glu
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Cys Gln Cys Val Pro Ser Lys Val Thr Lys Lys Tyr His Glu Val Leu
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Ser Thr Gly Gly
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 Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly Gly
 20 25 30

ggg cag aat cat cac gaa gtg gtg aag ttc atg gat gtc tat cag cgc 203
 Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln Arg
 35 40 45

agc tac tgc cat cca atc gag acc ctg gtg gac atc ttc cag gag tac 251
 Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu Tyr
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cct gat gag atc gag tac atc ttc aag cca tcc tgt gtg ccc ctg atg 299
 Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu Met
 70 75 80

cga tgc ggg ggc tgc tgc aat gac gag ggc ctg gag tgt gtg ccc act 347
 Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro Thr
 85 90 95

gag gag tcc aac atc acc atg cag att atg cgg atc aaa cct cac caa 395
Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His Gln
100 105 110

ggc cag cac ata gga gag atg agc ttc cta cag cac aac aaa tgt gaa 443
Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys Glu
115 120 125

tgc aga cca aag aaa gat aga gca aga caa gaa aat ccc tgt ggg cct 491
Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly Pro
130 135 140 145

tgc tca gag cgg aga aag cat ttg ttt gta caa gat ccg cag acg tgt 539
Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr Cys
150 155 160

aaa tgt tcc tgc aaa aac aca gac tcg cgt tgc aag gcg agg cag ctt 587
Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln Leu
165 170 175

gag tta aac gaa cgt act tgc aga tgt gac aag ccg agg cgg 629
Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg
180 185 190

tgagccgggc aggaggaagg agcctccctc agggtttcgg gaaccagatc tctcaccagg 689
aaagactgat acagaacgat cgatacagaa accacgctgc cgccaccaca ccatcaccat 749
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Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
35 40 45
Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
50 55 60
Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
65 70 75 80
Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly
130 135 140

Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr
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Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln
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Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg
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Met His
1

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Leu Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala Ala Leu
5 10 15

ctc ccg ggt cct cgc gag gcg ccc gcc gcc gcc gcc gcc ttc gag tcc 453
Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Ala Phe Glu Ser
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gga ctc gac ctc tcg gac gcg gag ccc gac gcg ggc gag gcc acg gct 501
Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala Thr Ala
35 40 45 50

tat gca agc aaa gat ctg gag gag cag tta cgg tct gtg tcc agt gta 549
Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser Ser Val
55 60 65

gat gaa ctc atg act gta ctc tac cca gaa tat tgg aaa atg tac aag 597
Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met Tyr Lys
70 75 80

tgt cag cta agg aaa gga ggc tgg caa cat aac aga gaa cag gcc aac	645
Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln Ala Asn	
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ctc aac tca agg aca gaa gag act ata aaa ttt gct gca gca cat tat	693
Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala His Tyr	
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aat aca gag atc ttg aaa agt att gat aat gag tgg aga aag act caa	741
Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln	
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Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe Gly Val	
135 140 145	
gcg aca aac acc ttc ttt aaa cct cca tgt gtg tcc gtc tac aga tgt	837
Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys	
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Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr	
165 170 175	
agc tac ctc agc aag acg tta ttt gaa att aca gtg cct ctc tct caa	933
Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln	
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Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg	
195 200 205 210	
tgc atg tct aaa ctg gat gtt tac aga caa gtt cat tcc att att aga	1029
Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile Ile Arg	
215 220 225	
cggt tcc ctg cca gca aca cta cca cag tgt cag gca gcg aac aag acc	1077
Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn Lys Thr	
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Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys Leu Ala	
245 250 255	
cag gaa gat ttt atg ttt tcc tgc gat gct gga gat gac tca aca gat	1173
Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser Thr Asp	
260 265 270	
gga ttc cat gac atc tgt gga cca aac aag gag ctg gat gaa gag acc	1221
Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu Glu Thr	
275 280 285 290	
tgt cag tgt gtc tgc aga gcg ggg ctt cgg cct gcc agc tgt gga ccc	1269
Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys Gly Pro	
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cac aaa gaa cta gac aga aac tca tgc cag tgt gtc tgt aaa aac aaa	1317
His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys Asn Lys	
310 315 320	
ctc ttc ccc agc caa tgt ggg gcc aac cga gaa ttt gat gaa aac aca	1365
Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu Asn Thr	
325 330 335	

tgc cag tgt gta tgt aaa aga acc tgc ccc aga aat caa ccc cta aat	1413
Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro Leu Asn	
340 345 350	
cct gga aaa tgt gcc tgt gaa tgt aca gaa agt cca cag aaa tgc ttg	1461
Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys Cys Leu	
355 360 365 370	
tta aaa gga aag aag ttc cac cac caa aca tgc agc tgt tac aga cgg	1509
Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr Arg Arg	
375 380 385	
cca tgt acg aac cgc cag aag gct tgt gag cca gga ttt tca tat agt	1557
Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser Tyr Ser	
390 395 400	
gaa gaa gtg tgt cgt tgt gtc cct tca tat tgg aaa aga cca caa atg	1605
Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Lys Arg Pro Gln Met	
405 410 415	
agc taagattgta ctgttttcca gttcatcgat tttctattat ggaaaactgt	1658
Ser	
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caaaagtctg tctttcctga accatgtgga taactttaca gaaatggact ggagctcatc	1778
tgcaaaaggc ctcttgtaaa gactgggtttt ctgccaatga ccaaacagcc aagattttcc	1838
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35 40 45
Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser
50 55 60
Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met
65 70 75 80
Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln
85 90 95
Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala
100 105 110

His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys
 115 120 125
 Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe
 130 135 140
 Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr
 145 150 155 160
 Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr
 165 170 175
 Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu
 180 185 190
 Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser
 195 200 205
 Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile
 210 215 220
 Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn
 225 230 235 240
 Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys
 245 250 255
 Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser
 260 265 270
 Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu
 275 280 285
 Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys
 290 295 300
 Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys
 305 310 315 320
 Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu
 325 330 335
 Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro
 340 345 350
 Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys
 355 360 365
 Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr
 370 375 380
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cccagccaca	gccttaccta	cgggctcctg	actccgcaag	gcttcagaa	gatgctcgaa	180														
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			Met	Pro	Val	Met	Arg	Leu	Phe	Pro	Cys	Phe								
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ctg	cag	ctc	ctg	gcc	ggg	ctg	gcg	ctg	cct	gct	gtg	ccc	ccc	cag	cag	399				
Leu	Gln	Leu	Leu	Ala	Gly	Leu	Ala	Leu	Pro	Ala	Val	Pro	Pro	Gln	Gln					
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tgg	gcc	ttg	tct	gct	ggg	aac	ggc	tcg	tca	gag	gtg	gaa	gtg	gta	ccc	447				
Trp	Ala	Leu	Ser	Ala	Gly	Asn	Gly	Ser	Ser	Glu	Val	Glu	Val	Val	Pro					
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ttc	cag	gaa	gtg	tgg	ggc	cgc	agc	tac	tgc	cgg	gcg	ctg	gag	agg	ctg	495				
Phe	Gln	Glu	Val	Trp	Gly	Arg	Ser	Tyr	Cys	Arg	Ala	Leu	Glu	Arg	Leu					
		45					50					55								
gtg	gac	gtc	gtg	tcc	gag	tac	ccc	agc	gag	gtg	gag	cac	atg	ttc	agc	543				
Val	Asp	Val	Val	Ser	Glu	Tyr	Pro	Ser	Glu	Val	Glu	His	Met	Phe	Ser					
	60					65					70									
cca	tcc	tgt	gtc	tcc	ctg	ctg	cgc	tgc	acc	ggc	tgc	tgc	ggc	gat	gag	591				
Pro	Ser	Cys	Val	Ser	Leu	Leu	Arg	Cys	Thr	Gly	Cys	Cys	Gly	Asp	Glu					
	75				80					85					90					
aat	ctg	cac	tgt	gtg	ccg	gtg	gag	acg	gcc	aat	gtc	acc	atg	cag	ctc	639				
Asn	Leu	His	Cys	Val	Pro	Val	Glu	Thr	Ala	Asn	Val	Thr	Met	Gln	Leu					
				95					100					105						
cta	aag	atc	cgt	tct	ggg	gac	cgg	ccc	tcc	tac	gtg	gag	ctg	acg	ttc	687				
Leu	Lys	Ile	Arg	Ser	Gly	Asp	Arg	Pro	Ser	Tyr	Val	Glu	Leu	Thr	Phe					
			110					115					120							
tct	cag	cac	gtt	cgc	tgc	gaa	tgc	cgg	cct	ctg	cgg	gag	aag	atg	aag	735				
Ser	Gln	His	Val	Arg	Cys	Glu	Cys	Arg	Pro	Leu	Arg	Glu	Lys	Met	Lys					
		125				130						135								
ccg	gaa	agg	tgc	ggc	gat	gct	gtt	ccc	cgg	agg	taaccacccc				cttggaggag	788				
Pro	Glu	Arg	Cys	Gly	Asp	Ala	Val	Pro	Arg	Arg										
	140					145														
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 Asn Gly Ser Ser Glu Val Glu Val Val Pro Phe Gln Glu Val Trp Gly
 35 40 45
 Arg Ser Tyr Cys Arg Ala Leu Glu Arg Leu Val Asp Val Val Ser Glu
 50 55 60
 Tyr Pro Ser Glu Val Glu His Met Phe Ser Pro Ser Cys Val Ser Leu
 65 70 75 80
 Leu Arg Cys Thr Gly Cys Cys Gly Asp Glu Asn Leu His Cys Val Pro
 85 90 95
 Val Glu Thr Ala Asn Val Thr Met Gln Leu Leu Lys Ile Arg Ser Gly
 100 105 110
 Asp Arg Pro Ser Tyr Val Glu Leu Thr Phe Ser Gln His Val Arg Cys
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 Ala Val Pro Arg Arg
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gctgcctgat gtcaactgct tagtaatcag tggatattga aatattcaaa atg tac 416																
Met Tyr 1																
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Arg Glu Trp Val Val Val Asn Val Phe Met Met Leu Tyr Val Gln Leu 5 10 15																
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Val Gln Gly Ser Ser Asn Glu His Gly Pro Val Lys Arg Ser Ser Gln 20 25 30																
tcc aca ttg gaa cga tct gaa cag cag atc agg gct gct tct agt ttg 560																
Ser Thr Leu Glu Arg Ser Glu Gln Gln Ile Arg Ala Ala Ser Ser Leu 35 40 45 50																
gag gaa cta ctt cga att act cac tct gag gac tgg aag ctg tgg aga 608																
Glu Glu Leu Leu Arg Ile Thr His Ser Glu Asp Trp Lys Leu Trp Arg 55 60 65																
tgc agg ctg agg ctc aaa agt ttt acc agt atg gac tct cgc tca gca 656																
Cys Arg Leu Arg Leu Lys Ser Phe Thr Ser Met Asp Ser Arg Ser Ala 70 75 80																
tcc cat cgg tcc act agg ttt gcg gca act ttc tat gac att gaa aca 704																
Ser His Arg Ser Thr Arg Phe Ala Ala Thr Phe Tyr Asp Ile Glu Thr 85 90 95																
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Leu Lys Val Ile Asp Glu Glu Trp Gln Arg Thr Gln Cys Ser Pro Arg 100 105 110																
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Glu Thr Cys Val Glu Val Ala Ser Glu Leu Gly Lys Ser Thr Asn Thr 115 120 125 130																
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Lys Gln Leu Phe Glu Ile Ser Val Pro Leu Thr Ser Val Pro Glu Leu	
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gtg cct gtt aaa gtt gcc aat cat aca ggt tgt aag tgc ttg cca aca	992
Val Pro Val Lys Val Ala Asn His Thr Gly Cys Lys Cys Leu Pro Thr	
180 185 190	
gcc ccc cgc cat cca tac tca att atc aga aga tcc atc cag atc cct	1040
Ala Pro Arg His Pro Tyr Ser Ile Ile Arg Arg Ser Ile Gln Ile Pro	
195 200 205 210	
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Glu Glu Asp Arg Cys Ser His Ser Lys Lys Leu Cys Pro Ile Asp Met	
215 220 225	
cta tgg gat agc aac aaa tgt aaa tgt gtt ttg cag gag gaa aat cca	1136
Leu Trp Asp Ser Asn Lys Cys Lys Cys Val Leu Gln Glu Glu Asn Pro	
230 235 240	
ctt gct gga aca gaa gac cac tct cat ctc cag gaa cca gct ctc tgt	1184
Leu Ala Gly Thr Glu Asp His Ser His Leu Gln Glu Pro Ala Leu Cys	
245 250 255	
ggg cca cac atg atg ttt gac gaa gat cgt tgc gag tgt gtc tgt aaa	1232
Gly Pro His Met Met Phe Asp Glu Asp Arg Cys Glu Cys Val Cys Lys	
260 265 270	
aca cca tgt ccc aaa gat cta atc cag cac ccc aaa aac tgc agt tgc	1280
Thr Pro Cys Pro Lys Asp Leu Ile Gln His Pro Lys Asn Cys Ser Cys	
275 280 285 290	
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Phe Glu Cys Lys Glu Ser Leu Glu Thr Cys Cys Gln Lys His Lys Leu	
295 300 305	
ttt cac cca gac acc tgc agc tgt gag gac aga tgc ccc ttt cat acc	1376
Phe His Pro Asp Thr Cys Ser Cys Glu Asp Arg Cys Pro Phe His Thr	
310 315 320	
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Arg Pro Cys Ala Ser Gly Lys Thr Ala Cys Ala Lys His Cys Arg Phe	
325 330 335	
cca aag gag aaa agg gct gcc cag ggg ccc cac agc cga aag aat cct	1472
Pro Lys Glu Lys Arg Ala Ala Gln Gly Pro His Ser Arg Lys Asn Pro	
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gtgaatccag accaaccttc cattcacacc agctaaggag tccctgggttc attgatggat	1652
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tggcaggtgt catatgactg attactcaga gcagatgagg aaaactgtag tctctgagtc	1832

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tatgatcagt actgactttc tgattactgt ccagcttata gtcttccagt ttaatgaact 1952
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aaaaaaaaaa aaaaaaa 2029

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35 40 45
Ser Leu Glu Glu Leu Leu Arg Ile Thr His Ser Glu Asp Trp Lys Leu
50 55 60
Trp Arg Cys Arg Leu Arg Leu Lys Ser Phe Thr Ser Met Asp Ser Arg
65 70 75 80
Ser Ala Ser His Arg Ser Thr Arg Phe Ala Ala Thr Phe Tyr Asp Ile
85 90 95
Glu Thr Leu Lys Val Ile Asp Glu Glu Trp Gln Arg Thr Gln Cys Ser
100 105 110
Pro Arg Glu Thr Cys Val Glu Val Ala Ser Glu Leu Gly Lys Ser Thr
115 120 125
Asn Thr Phe Phe Lys Pro Pro Cys Val Asn Val Phe Arg Cys Gly Gly
130 135 140
Cys Cys Asn Glu Glu Ser Leu Ile Cys Met Asn Thr Ser Thr Ser Tyr
145 150 155 160
Ile Ser Lys Gln Leu Phe Glu Ile Ser Val Pro Leu Thr Ser Val Pro
165 170 175
Glu Leu Val Pro Val Lys Val Ala Asn His Thr Gly Cys Lys Cys Leu
180 185 190
Pro Thr Ala Pro Arg His Pro Tyr Ser Ile Ile Arg Arg Ser Ile Gln
195 200 205
Ile Pro Glu Glu Asp Arg Cys Ser His Ser Lys Lys Leu Cys Pro Ile
210 215 220
Asp Met Leu Trp Asp Ser Asn Lys Cys Lys Cys Val Leu Gln Glu Glu
225 230 235 240
Asn Pro Leu Ala Gly Thr Glu Asp His Ser His Leu Gln Glu Pro Ala
245 250 255

Leu Cys Gly Pro His Met Met Phe Asp Glu Asp Arg Cys Glu Cys Val
 260 265 270
 Cys Lys Thr Pro Cys Pro Lys Asp Leu Ile Gln His Pro Lys Asn Cys
 275 280 285
 Ser Cys Phe Glu Cys Lys Glu Ser Leu Glu Thr Cys Cys Gln Lys His
 290 295 300
 Lys Leu Phe His Pro Asp Thr Cys Ser Cys Glu Asp Arg Cys Pro Phe
 305 310 315 320
 His Thr Arg Pro Cys Ala Ser Gly Lys Thr Ala Cys Ala Lys His Cys
 325 330 335
 Arg Phe Pro Lys Glu Lys Arg Ala Ala Gln Gly Pro His Ser Arg Lys
 340 345 350

Asn Pro

<210> 19
 <211> 1830
 <212> DNA
 <213> Orf virus

<220>
 <221> CDS
 <222> (312)..(755)

<400> 19
 cggccacgcg gccgcgaact gcgcgctcgc gcgcgtggcg accgcgctga cgcgccgcgt 60
 gccgcgcgagc cggcacggcc tcgcggaggg cggcacgccg ccgtggacgc tgctgctggc 120
 ggtggccgcg gtggcggtgc tcggcggtgt ggcaatttcg ctgctgcgcc gcgcgctaag 180
 aatacggttt agatactcaa agtctatcca gacacttaga gtgtaacttt gagtaaaaaa 240
 tgtaaatact aacgccaaaa ttctgatagt tgtaagcaa tatataacat ttttaaaacg 300
 tcataccagg c atg aag tta aca gct acg tta caa gtt gtt gtt gca ttg 350
 Met Lys Leu Thr Ala Thr Leu Gln Val Val Val Ala Leu
 1 5 10
 tta ata tgt atg tat aat ttg cca gaa tgc gtg tct cag agt aat gat 398
 Leu Ile Cys Met Tyr Asn Leu Pro Glu Cys Val Ser Gln Ser Asn Asp
 15 20 25
 tca cct cct tca acc aat gac tgg atg cgt aca cta gac aaa agt ggt 446
 Ser Pro Pro Ser Thr Asn Asp Trp Met Arg Thr Leu Asp Lys Ser Gly
 30 35 40 45
 tgt aaa cct aga gat act gtt gtt tat ttg gga gaa gaa tat cca gaa 494
 Cys Lys Pro Arg Asp Thr Val Val Tyr Leu Gly Glu Glu Tyr Pro Glu
 50 55 60
 agc act aac cta caa tat aat ccc cgg tgc gta act gtt aaa cga tgc 542
 Ser Thr Asn Leu Gln Tyr Asn Pro Arg Cys Val Thr Val Lys Arg Cys
 65 70 75
 agt ggt tgc tgt aac ggt gac ggt caa ata tgt aca gcg gtt gaa aca 590
 Ser Gly Cys Cys Asn Gly Asp Gly Gln Ile Cys Thr Ala Val Glu Thr
 80 85 90

aga aat aca act gta aca gtt tca gta acc ggc gtg tct agt tcg tct 638
 Arg Asn Thr Thr Val Thr Val Ser Val Thr Gly Val Ser Ser Ser Ser
 95 100 105

ggt act aat agt ggt gta tct act aac ctt caa aga ata agt gtt aca 686
 Gly Thr Asn Ser Gly Val Ser Thr Asn Leu Gln Arg Ile Ser Val Thr
 110 115 120 125

gaa cac aca aag tgc gat tgt att ggt aga aca acg aca aca cct acg 734
 Glu His Thr Lys Cys Asp Cys Ile Gly Arg Thr Thr Thr Thr Pro Thr
 130 135 140

acc act agg gaa cct aga cga taactaataa caaaaaatgt ttatttttgt 785
 Thr Thr Arg Glu Pro Arg Arg
 145

aaataacttaa ttattacaca ctttacaata atctcaaaaa taaattgcgt gcccgacgg 845

ctgcagctgg tgacgctgct gtgtcacaca ctgcgtattc gattcaagtt cactaacgcc 905

actaaactag ttgtgcgtgt ccgagtgtta accgtacgtc aaactaacat cttacctgtc 965

cgtgacaaga actaaaactt gaaccacata tttttaagt atatttaaca aaatcactca 1025

cactcacaca atcataaaca ccacaaccac aaccaaacac gcatgagaat taatattctt 1085

acttatccgt aacactctat gctgtacatc aacgcatcag agcagtctga gtctgactaa 1145

tggcggcaaa cgggaacgca ggcgcgacat aatcactgag aatctccgca gcaaccgctc 1205

aaggacatct ctagcgctaa cggctgtttg tcattcccc gtgtgttcat ctcacacgac 1265

attgtgaccg tcgcaaagca cacattcaaa gtgccgcatg tggaagaatt caccgtcgag 1325

acacacacca taattaaaca agatcagtgc ataagagaga ttagcattct acagcacacc 1385

acgtgcgaat acggacctcg taattgttta gactagaaca cctctggtct aaacaacatg 1445

tccgatctta gaacagagtt tatgacgcat atgtaactgt gttctttatg tagaagttat 1505

cttttatgtc actcccttgt cttagatgag ttatacatga catgatgtat gtgtcgcccc 1565

cggcggcgcg gggcgctcgg cggcggggct gctgcgcgcg gcgggcccgc ggtggcggcg 1625

gctggcgcg cgctgcggcc gcgggcgcgc ggcggggtag cggcccgcgc gcccgggcg 1685

ccgccgcagc ccttgccccg gaccaggcgc cacggagcaa agtgaaaaag gaccgcctag 1745

cagtcgagac cctcccgccg cagccgcgac accccacacc cgccttcac ccgccagacg 1805

ccaacaccac agccaacaag catgc 1830

<210> 20
 <211> 148
 <212> PRT
 <213> Orf virus

<400> 20
 Met Lys Leu Thr Ala Thr Leu Gln Val Val Val Ala Leu Leu Ile Cys
 1 5 10 15

Met Tyr Asn Leu Pro Glu Cys Val Ser Gln Ser Asn Asp Ser Pro Pro
20 25 30

Ser Thr Asn Asp Trp Met Arg Thr Leu Asp Lys Ser Gly Cys Lys Pro
35 40 45

Arg Asp Thr Val Val Tyr Leu Gly Glu Glu Tyr Pro Glu Ser Thr Asn
50 55 60

Leu Gln Tyr Asn Pro Arg Cys Val Thr Val Lys Arg Cys Ser Gly Cys
65 70 75 80

Cys Asn Gly Asp Gly Gln Ile Cys Thr Ala Val Glu Thr Arg Asn Thr
85 90 95

Thr Val Thr Val Ser Val Thr Gly Val Ser Ser Ser Ser Gly Thr Asn
100 105 110

Ser Gly Val Ser Thr Asn Leu Gln Arg Ile Ser Val Thr Glu His Thr
115 120 125

Lys Cys Asp Cys Ile Gly Arg Thr Thr Thr Thr Pro Thr Thr Thr Arg
130 135 140

Glu Pro Arg Arg
145

<210> 21
<211> 851
<212> DNA
<213> Orf virus

<220>
<221> CDS
<222> (2)..(223)

<400> 21
c ggc cac gcg gcc gcg aac tgc gcg ctc gcg cgc gtg gcg acc gcg ctg 49
Gly His Ala Ala Ala Asn Cys Ala Leu Ala Arg Val Ala Thr Ala Leu
1 5 10 15

acg cgc cgc gtg ccc gcg agc cgg cac ggc ctc gcg gag ggc ggc acg 97
Thr Arg Arg Val Pro Ala Ser Arg His Gly Leu Ala Glu Gly Gly Thr
20 25 30

ccg ccg tgg acg ctg ctg ctg gcg gtg gcc gcg gtg acg gtg ctc ggc 145
Pro Pro Trp Thr Leu Leu Leu Ala Val Ala Ala Val Thr Val Leu Gly
35 40 45

gtg gtg gcg gtt tca ctg ctg cgg cgc gcg ctg cgg gta cgc tac cgc 193
Val Val Ala Val Ser Leu Leu Arg Arg Ala Leu Arg Val Arg Tyr Arg
50 55 60

ttc gcg cgg ccg gcc gcg ctg cgc gcg tag ccgcgcaaaa tgtaaattat 243
Phe Ala Arg Pro Ala Ala Leu Arg Ala
65 70

aacgccaac ttttaagggg gaggcgccat gaagttgctc gtcggcatat tagtagccgt 303
gtgcttgac cagtatctgc tgaacgcgga cagcaacacg aaaggatggt ccgaagtgct 363

gaaaggcagc gaggcgcaagc ctaggccgat tggtgttcct gtaagcgaga cgcacccaga 423
 gctgacttct cagcggttca acccgccgtg tggtcacgttg atgcgatgcg gcgggtgctg 483
 caacgacgag agcttggaat gcgtccccac ggaagaagta aacgtgagca tggaactcct 543
 gggggcgctg ggctccggtg gtaacgggat gcaacgtctg agcttcgtag agcataagaa 603
 atgcgattgt agaccacgat tcacaaccac gccaccgacg accacaaggc cgcccagaag 663
 acgccgctag aactttttat ggaccgcaga tccaaacgat ggatgcatc aggtacatgc 723
 ggaagaaggc gccacggagc aaagtgaaaa aggaccgcct agcagtcgag accctccgc 783
 cgcagccgcg gacacccac acccgcttc caccgcgag acgccaacac cgcagccaac 843
 aagcatgc 851

<210> 22
 <211> 73
 <212> PRT
 <213> Orf virus

<400> 22
 Gly His Ala Ala Ala Asn Cys Ala Leu Ala Arg Val Ala Thr Ala Leu
 1 5 10 15
 Thr Arg Arg Val Pro Ala Ser Arg His Gly Leu Ala Glu Gly Gly Thr
 20 25 30
 Pro Pro Trp Thr Leu Leu Leu Ala Val Ala Ala Val Thr Val Leu Gly
 35 40 45
 Val Val Ala Val Ser Leu Leu Arg Arg Ala Leu Arg Val Arg Tyr Arg
 50 55 60
 Phe Ala Arg Pro Ala Ala Leu Arg Ala
 65 70

<210> 23
 <211> 2305
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (404)..(991)

<400> 23
 ttcttggggc tgatgtccgc aaatatgcag aattaccggc cgggtcgctc ctgaagccag 60
 cgcggggagc gagcgggcg gcggccagca ccgggaacgc accgaggaag aagcccagcc 120
 cccgccctcc gccccttcg tccccacccc ctaccggcg gccaggagg ctccccggct 180
 gcggcgcgca ctccctgttt ctctcctcc tggctggcg tgctgcctc tccgcactca 240
 ctgctgcgcg ggcgcgctcc gccagctccg tgctccccgc gccaccctcc tccgggcccgc 300

gctccctaag ggatggtact gaatttcgcc gccacaggag accggctgga ggcgccgccc 360
cgcgccctgc ctctcctcgc agcagccagc gcctcggggac gcg atg agg acc ttg 415
Met Arg Thr Leu
1
gct tgc ctg ctg ctc ctc ggc tgc gga tac ctc gcc cat gtt ctg gcc 463
Ala Cys Leu Leu Leu Leu Gly Cys Gly Tyr Leu Ala His Val Leu Ala
5 10 15 20
gag gaa gcc gag atc ccc cgc gag gtg atc gag agg ctg gcc cgc agt 511
Glu Glu Ala Glu Ile Pro Arg Glu Val Ile Glu Arg Leu Ala Arg Ser
25 30 35
cag atc cac agc atc cgg gac ctc cag cga ctc ctg gag ata gac tcc 559
Gln Ile His Ser Ile Arg Asp Leu Gln Arg Leu Leu Glu Ile Asp Ser
40 45 50
gta ggg agt gag gat tct ttg gac acc agc ctg aga gct cac ggg gtc 607
Val Gly Ser Glu Asp Ser Leu Asp Thr Ser Leu Arg Ala His Gly Val
55 60 65
cac gcc act aag cat gtg ccc gag aag cgg ccc ctg ccc att cgg agg 655
His Ala Thr Lys His Val Pro Glu Lys Arg Pro Leu Pro Ile Arg Arg
70 75 80
aag aga agc atc gag gaa gct gtc ccc gct gtc tgc aag acc agg acg 703
Lys Arg Ser Ile Glu Glu Ala Val Pro Ala Val Cys Lys Thr Arg Thr
85 90 95 100
gtc att tac gag att cct cgg agt cag gtc gac ccc acg tcc gcc aac 751
Val Ile Tyr Glu Ile Pro Arg Ser Gln Val Asp Pro Thr Ser Ala Asn
105 110 115
ttc ctg atc tgg ccc ccg tgc gtg gag gtg aaa cgc tgc acc ggc tgc 799
Phe Leu Ile Trp Pro Pro Cys Val Glu Val Lys Arg Cys Thr Gly Cys
120 125 130
tgc aac acg agc agt gtc aag tgc cag ccc tcc cgc gtc cac cac cgc 847
Cys Asn Thr Ser Ser Val Lys Cys Gln Pro Ser Arg Val His His Arg
135 140 145
agc gtc aag gtg gcc aag gtg gaa tac gtc agg aag aag cca aaa tta 895
Ser Val Lys Val Ala Lys Val Glu Tyr Val Arg Lys Lys Pro Lys Leu
150 155 160
aaa gaa gtc cag gtg agg tta gag gag cat ttg gag tgc gcc tgc gcg 943
Lys Glu Val Gln Val Arg Leu Glu Glu His Leu Glu Cys Ala Cys Ala
165 170 175 180
acc aca agc ctg aat ccg gat tat cgg gaa gag gac acg gat gtg agg 991
Thr Thr Ser Leu Asn Pro Asp Tyr Arg Glu Glu Asp Thr Asp Val Arg
185 190 195
tgaggatgag ccgcagccct ttccctggggac atggatgtac atggcgtggt acattcctga 1051
acctactatg tacggtgctt tattgccagt gtgcggtctt tggtctcctc cgtgaaaaac 1111
tgtgtccgag aacactcggg agaacaaaga gacagtgcac atttgtttaa tgtgacatca 1171
aagcaagtat tgtagcactc ggtgaagcag taagaagctt ccttgtcaaa aagagagaga 1231

gagagagaga gagagaaaac aaaaccacaa atgacaaaaa caaaacggac tcacaaaaat 1291
atctaaactc gatgagatgg agggctgccc cgtgggatgg aagtgcagag gtctcagcag 1351
actggatttc tgtccgggtg gtcacagggtg cttttttgcc gaggatgcag agcctgcttt 1411
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ttggaaaccg ccacgcgaac tttagaaacc acacctctc gctgtagtat ttaagcccat 1531
acagaaacct tcctgagagc ctttaagtgg tttttttttt gtttttgttt tgtttttttt 1591
ttttttgttt tttttttttt tttttttttt tacaccataa agtgattatt aagcttcctt 1651
ttactctttg gctagctttt tttttttttt tttttttttt tttttttaat tatctcttgg 1711
atgacattta caccgataac acacaggctg ctgtaactgt caggacagtg cgacgggtatt 1771
tttcctagca agatgcaaac taatgagatg tattaataa aacatggat acctacctat 1831
gcatcatttc ctaaagtgtt ctggctttgt gtttctccct taccctgctt tatttgtaa 1891
tttaagccat tttgaaagaa ctatgcgtca accaatcgta cgccgtccct gcggcacctg 1951
ccccagagcc cgtttgtggc tgagtgacaa cttgttcccc gcagtgcaca cctagaatgc 2011
tgtgttccca cgcggcacgt gagatgcatt gccgcttctg tctgtgttgt tgggtgtgcc 2071
tgggtgccgtg gtggcgggtca ctccctctgc tgccagtgtt tggacagaac ccaaattctt 2131
tatttttggg aagatattgt gctttacctg tattaacaga aatgtgtgtg tgtggtttgt 2191
ttttttgtaa aggtgaagtt tgtatgttta cctaataatta cctgttttgt atacctgaga 2251
gcctgctatg ttcttctttt gttgatccaa aattaaanaa aaaataccac caac 2305

<210> 24
<211> 196
<212> PRT
<213> Homo sapiens

<400> 24
Met Arg Thr Leu Ala Cys Leu Leu Leu Leu Gly Cys Gly Tyr Leu Ala
1 5 10 15
His Val Leu Ala Glu Glu Ala Glu Ile Pro Arg Glu Val Ile Glu Arg
20 25 30
Leu Ala Arg Ser Gln Ile His Ser Ile Arg Asp Leu Gln Arg Leu Leu
35 40 45
Glu Ile Asp Ser Val Gly Ser Glu Asp Ser Leu Asp Thr Ser Leu Arg
50 55 60
Ala His Gly Val His Ala Thr Lys His Val Pro Glu Lys Arg Pro Leu
65 70 75 80
Pro Ile Arg Arg Lys Arg Ser Ile Glu Glu Ala Val Pro Ala Val Cys
85 90 95
Lys Thr Arg Thr Val Ile Tyr Glu Ile Pro Arg Ser Gln Val Asp Pro
100 105 110

Thr Ser Ala Asn Phe Leu Ile Trp Pro Pro Cys Val Glu Val Lys Arg
 115 120 125
 Cys Thr Gly Cys Cys Asn Thr Ser Ser Val Lys Cys Gln Pro Ser Arg
 130 135 140
 Val His His Arg Ser Val Lys Val Ala Lys Val Glu Tyr Val Arg Lys
 145 150 155 160
 Lys Pro Lys Leu Lys Glu Val Gln Val Arg Leu Glu Glu His Leu Glu
 165 170 175
 Cys Ala Cys Ala Thr Thr Ser Leu Asn Pro Asp Tyr Arg Glu Glu Asp
 180 185 190
 Thr Asp Val Arg
 195

<210> 25
 <211> 2137
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (983)..(1705)

<400> 25
 cctgctgc ctccctgcgc acccgcagcc tccccgctg cctccctagg gctcccctcc 60
 ggccgccagc gccattttt cattccctag atagagatac tttgcgcgca cacacataca 120
 tacgcgcgca aaaaggaaaa aaaaaaaaaa aagcccaccc tccagcctcg ctgcaaagag 180
 aaaaccggag cagccgcagc tcgcagctcg cagcccgag cccgcagagg acgcccagag 240
 cggcgagcgg gcgggcagac ggaccgacgg actcgcgcgcg cgtccacctg tcggccgggc 300
 ccagccgagc gcgcagcggg cacgccgcgc gcgcggagca gccgtgccc cgcgccgggc 360
 ccgcgccag ggcgcacacg ctcccgcccc cctaccggc ccgggcggga gtttgcacct 420
 ctccctgccc gggtgctcga gctgccgttg caaagccaac tttggaaaaa gttttttggg 480
 ggagacttgg gccttgaggt gcccagctcc gcgctttccg attttggggg cctttccaga 540
 aaatgttgca aaaaagctaa gccggcgggc agaggaaaac gcctgtagcc ggcgagtga 600
 gacgaaccat cgactgccgt gttccttttc ctcttgagg ttggagtccc ctgggcgccc 660
 ccacacggct agacgcctcg gctggttcgc gacgcagccc cccggccgtg gatgctgcac 720
 tcgggctcgg gatccgccc ggtagcggcc tcggaccag gtcttgcgc caggtcctcc 780
 cctgcccccc agcgacggag ccggggccgg gggcggcggc gccgggggca tgcgggtgag 840
 ccgcggctgc agaggcctga gcgcctgatc gccgcggacc cgagccgagc ccacccccct 900
 ccccagcccc ccaccctggc cgcggggggc gcgcgctcga tctacgcgtt cggggccccg 960

cggggccggg cccggagtcg gc atg aat cgc tgc tgg gcg ctc ttc ctg tct	1012
Met Asn Arg Cys Trp Ala Leu Phe Leu Ser	
1 5 10	
ctc tgc tgc tac ctg cgt ctg gtc agc gcc gag ggg gac ccc att ccc	1060
Leu Cys Cys Tyr Leu Arg Leu Val Ser Ala Glu Gly Asp Pro Ile Pro	
15 20 25	
gag gag ctt tat gag atg ctg agt gac cac tcg atc cgc tcc ttt gat	1108
Glu Glu Leu Tyr Glu Met Leu Ser Asp His Ser Ile Arg Ser Phe Asp	
30 35 40	
gat ctc caa cgc ctg ctg cac gga gac ccc gga gag gaa gat ggg gcc	1156
Asp Leu Gln Arg Leu Leu His Gly Asp Pro Gly Glu Glu Asp Gly Ala	
45 50 55	
gag ttg gac ctg aac atg acc cgc tcc cac tct gga ggc gag ctg gag	1204
Glu Leu Asp Leu Asn Met Thr Arg Ser His Ser Gly Gly Glu Leu Glu	
60 65 70	
agc ttg gct cgt gga aga agg agc ctg ggt tcc ctg acc att gct gag	1252
Ser Leu Ala Arg Gly Arg Arg Ser Leu Gly Ser Leu Thr Ile Ala Glu	
75 80 85 90	
ccg gcc atg atc gcc gag tgc aag acg cgc acc gag gtg ttc gag atc	1300
Pro Ala Met Ile Ala Glu Cys Lys Thr Arg Thr Glu Val Phe Glu Ile	
95 100 105	
tcc cgg cgc ctc ata gac cgc acc aac gcc aac ttc ctg gtg tgg ccg	1348
Ser Arg Arg Leu Ile Asp Arg Thr Asn Ala Asn Phe Leu Val Trp Pro	
110 115 120	
ccc tgt gtg gag gtg cag cgc tgc tcc ggc tgc tgc aac aac cgc aac	1396
Pro Cys Val Glu Val Gln Arg Cys Ser Gly Cys Cys Asn Asn Arg Asn	
125 130 135	
gtg cag tgc cgc ccc acc cag gtg cag ctg cga cct gtc cag gtg aga	1444
Val Gln Cys Arg Pro Thr Gln Val Gln Leu Arg Pro Val Gln Val Arg	
140 145 150	
aag atc gag att gtg cgg aag aag cca atc ttt aag aag gcc acg gtg	1492
Lys Ile Glu Ile Val Arg Lys Lys Pro Ile Phe Lys Lys Ala Thr Val	
155 160 165 170	
acg ctg gaa gac cac ctg gca tgc aag tgt gag aca gtg gca gct gca	1540
Thr Leu Glu Asp His Leu Ala Cys Lys Cys Glu Thr Val Ala Ala Ala	
175 180 185	
cgg cct gtg acc cga agc ccg ggg ggt tcc cag gag cag cga gcc aaa	1588
Arg Pro Val Thr Arg Ser Pro Gly Gly Ser Gln Glu Gln Arg Ala Lys	
190 195 200	
acg ccc caa act cgg gtg acc att cgg acg gtg cga gtc cgc cgg ccc	1636
Thr Pro Gln Thr Arg Val Thr Ile Arg Thr Val Arg Val Arg Arg Pro	
205 210 215	
ccc aag ggc aag cac cgg aaa ttc aag cac acg cat gac aag acg gca	1684
Pro Lys Gly Lys His Arg Lys Phe Lys His Thr His Asp Lys Thr Ala	
220 225 230	

ctg aag gag acc ctt gga gcc taggggcatc ggcaggagag tgtgtgggca 1735
 Leu Lys Glu Thr Leu Gly Ala
 235 240

gggttatttta atatggtatt tgctgtattg ccccatggg gccttgaggat agataatatt 1795
 gtttcctctg tccgtctgtc tcgatgctg attcggacgg ccaatggtgc ctccccacc 1855
 cctccacgtg tccgtccacc cttccatcag cgggtctcct cccagcggcc tccggctctt 1915
 gcccagcagc tcaagaagaa aaagaaggac tgaactccat cgccatcttc ttcccttaac 1975
 tccaagaact tgggataaga gtgtgagaga gactgatggg gtcgctcttt gggggaaacg 2035
 gggtccttcc cctgcacctg gcctgggcca cacctgagcg ctgtggactg tcttgaggag 2095
 ccctgaggac ctctcagcat agcctgctg atccctgaac cc 2137

<210> 26
 <211> 241
 <212> PRT
 <213> Homo sapiens

<400> 26
 Met Asn Arg Cys Trp Ala Leu Phe Leu Ser Leu Cys Cys Tyr Leu Arg
 1 5 10 15
 Leu Val Ser Ala Glu Gly Asp Pro Ile Pro Glu Glu Leu Tyr Glu Met
 20 25 30
 Leu Ser Asp His Ser Ile Arg Ser Phe Asp Asp Leu Gln Arg Leu Leu
 35 40 45
 His Gly Asp Pro Gly Glu Glu Asp Gly Ala Glu Leu Asp Leu Asn Met
 50 55 60
 Thr Arg Ser His Ser Gly Gly Glu Leu Glu Ser Leu Ala Arg Gly Arg
 65 70 75 80
 Arg Ser Leu Gly Ser Leu Thr Ile Ala Glu Pro Ala Met Ile Ala Glu
 85 90 95
 Cys Lys Thr Arg Thr Glu Val Phe Glu Ile Ser Arg Arg Leu Ile Asp
 100 105 110
 Arg Thr Asn Ala Asn Phe Leu Val Trp Pro Pro Cys Val Glu Val Gln
 115 120 125
 Arg Cys Ser Gly Cys Cys Asn Asn Arg Asn Val Gln Cys Arg Pro Thr
 130 135 140
 Gln Val Gln Leu Arg Pro Val Gln Val Arg Lys Ile Glu Ile Val Arg
 145 150 155 160
 Lys Lys Pro Ile Phe Lys Lys Ala Thr Val Thr Leu Glu Asp His Leu
 165 170 175
 Ala Cys Lys Cys Glu Thr Val Ala Ala Arg Pro Val Thr Arg Ser
 180 185 190
 Pro Gly Gly Ser Gln Glu Gln Arg Ala Lys Thr Pro Gln Thr Arg Val
 195 200 205

Thr Ile Arg Thr Val Arg Val Arg Arg Pro Pro Lys Gly Lys His Arg
 210 215 220
 Lys Phe Lys His Thr His Asp Lys Thr Ala Leu Lys Glu Thr Leu Gly
 225 230 235 240

Ala

<210> 27
 <211> 3007
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (492)..(1529)

<400> 27
 gcccgagag ccgcatttat tggcagcttt gttattgatc agaaactgct cgccgccgac 60
 ttggcttcca gtctggctgc gggcaaccct tgagttttcg cctctgtcct gtcccccgaa 120
 ctgacaggtg ctcccagcaa cttgctgggg acttctcgcc gctccccgc gtccccaccc 180
 cctcattcct ccctcgctt cccccacc ccaccactt cgccacagct caggatttgt 240
 ttaaacttg ggaaactggt tcaggtccag gttttgcttt gatccttttc aaaaactgga 300
 gacacagaag agggctctag gaaaaagttt tggatgggat tatgtggaaa ctaccctgcg 360
 attctctgct gccagagcag gctcggcgct tccacccag tgcagccttc ccctggcggt 420
 ggtgaaagag actcgggagt cgctgcttcc aaagtgccg ccgtgagtga gctctaccc 480
 cagtcagcca a atg agc ctc ttc ggg ctt ctc ctg ctg aca tct gcc ctg 530
 Met Ser Leu Phe Gly Leu Leu Leu Leu Thr Ser Ala Leu
 1 5 10
 gcc ggc cag aga cag ggg act cag gcg gaa tcc aac ctg agt agt aaa 578
 Ala Gly Gln Arg Gln Gly Thr Gln Ala Glu Ser Asn Leu Ser Ser Lys
 15 20 25
 ttc cag ttt tcc agc aac aag gaa cag aac gga gta caa gat cct cag 626
 Phe Gln Phe Ser Ser Asn Lys Glu Gln Asn Gly Val Gln Asp Pro Gln
 30 35 40 45
 cat gag aga att att act gtg tct act aat gga agt att cac agc cca 674
 His Glu Arg Ile Ile Thr Val Ser Thr Asn Gly Ser Ile His Ser Pro
 50 55 60
 agg ttt cct cat act tat cca aga aat acg gtc ttg gta tgg aga tta 722
 Arg Phe Pro His Thr Tyr Pro Arg Asn Thr Val Leu Val Trp Arg Leu
 65 70 75
 gta gca gta gag gaa aat gta tgg ata caa ctt acg ttt gat gaa aga 770
 Val Ala Val Glu Glu Asn Val Trp Ile Gln Leu Thr Phe Asp Glu Arg
 80 85 90
 ttt ggg ctt gaa gac cca gaa gat gac ata tgc aag tat gat ttt gta 818
 Phe Gly Leu Glu Asp Pro Glu Asp Asp Ile Cys Lys Tyr Asp Phe Val
 95 100 105

gaa gtt gag gaa ccc agt gat gga act ata tta ggg cgc tgg tgt ggt Glu Val Glu Glu Pro Ser Asp Gly Thr Ile Leu Gly Arg Trp Cys Gly 110 115 120 125	866
tct ggt act gta cca gga aaa cag att tct aaa gga aat caa att agg Ser Gly Thr Val Pro Gly Lys Gln Ile Ser Lys Gly Asn Gln Ile Arg 130 135 140	914
ata aga ttt gta tct gat gaa tat ttt cct tct gaa cca ggg ttc tgc Ile Arg Phe Val Ser Asp Glu Tyr Phe Pro Ser Glu Pro Gly Phe Cys 145 150 155	962
atc cac tac aac att gtc atg cca caa ttc aca gaa gct gtg agt cct Ile His Tyr Asn Ile Val Met Pro Gln Phe Thr Glu Ala Val Ser Pro 160 165 170	1010
tca gtg cta ccc cct tca gct ttg cca ctg gac ctg ctt aat aat gct Ser Val Leu Pro Pro Ser Ala Leu Pro Leu Asp Leu Leu Asn Asn Ala 175 180 185	1058
ata act gcc ttt agt acc ttg gaa gac ctt att cga tat ctt gaa cca Ile Thr Ala Phe Ser Thr Leu Glu Asp Leu Ile Arg Tyr Leu Glu Pro 190 195 200 205	1106
gag aga tgg cag ttg gac tta gaa gat cta tat agg cca act tgg caa Glu Arg Trp Gln Leu Asp Leu Glu Asp Leu Tyr Arg Pro Thr Trp Gln 210 215 220	1154
ctt ctt ggc aag gct ttt gtt ttt gga aga aaa tcc aga gtg gtg gat Leu Leu Gly Lys Ala Phe Val Phe Gly Arg Lys Ser Arg Val Val Asp 225 230 235	1202
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aac ttc tca gtg tcc ata agg gaa gaa cta aag aga acc gat acc att Asn Phe Ser Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile 255 260 265	1298
ttc tgg cca ggt tgt ctc ctg gtt aaa cgc tgt ggt ggg aac tgt gcc Phe Trp Pro Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala 270 275 280 285	1346
tgt tgt ctc cac aat tgc aat gaa tgt caa tgt gtc cca agc aaa gtt Cys Cys Leu His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser Lys Val 290 295 300	1394
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agg gga ttg cac aaa tca ctc acc gac gtg gcc ctg gag cac cat gag Arg Gly Leu His Lys Ser Leu Thr Asp Val Ala Leu Glu His His Glu 320 325 330	1490
gag tgt gac tgt gtg tgc aga ggg agc aca gga gga tag ccgcacacc Glu Cys Asp Cys Val Cys Arg Gly Ser Thr Gly Gly 335 340 345	1539

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<210> 28
 <211> 345
 <212> PRT
 <213> Homo sapiens

<400> 28
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 Arg Gln Gly Thr Gln Ala Glu Ser Asn Leu Ser Ser Lys Phe Gln Phe
 20 25 30

Ser Ser Asn Lys Glu Gln Asn Gly Val Gln Asp Pro Gln His Glu Arg
 35 40 45
 Ile Ile Thr Val Ser Thr Asn Gly Ser Ile His Ser Pro Arg Phe Pro
 50 55 60
 His Thr Tyr Pro Arg Asn Thr Val Leu Val Trp Arg Leu Val Ala Val
 65 70 75 80
 Glu Glu Asn Val Trp Ile Gln Leu Thr Phe Asp Glu Arg Phe Gly Leu
 85 90 95
 Glu Asp Pro Glu Asp Asp Ile Cys Lys Tyr Asp Phe Val Glu Val Glu
 100 105 110
 Glu Pro Ser Asp Gly Thr Ile Leu Gly Arg Trp Cys Gly Ser Gly Thr
 115 120 125
 Val Pro Gly Lys Gln Ile Ser Lys Gly Asn Gln Ile Arg Ile Arg Phe
 130 135 140
 Val Ser Asp Glu Tyr Phe Pro Ser Glu Pro Gly Phe Cys Ile His Tyr
 145 150 155 160
 Asn Ile Val Met Pro Gln Phe Thr Glu Ala Val Ser Pro Ser Val Leu
 165 170 175
 Pro Pro Ser Ala Leu Pro Leu Asp Leu Leu Asn Asn Ala Ile Thr Ala
 180 185 190
 Phe Ser Thr Leu Glu Asp Leu Ile Arg Tyr Leu Glu Pro Glu Arg Trp
 195 200 205
 Gln Leu Asp Leu Glu Asp Leu Tyr Arg Pro Thr Trp Gln Leu Leu Gly
 210 215 220
 Lys Ala Phe Val Phe Gly Arg Lys Ser Arg Val Val Asp Leu Asn Leu
 225 230 235 240
 Leu Thr Glu Glu Val Arg Leu Tyr Ser Cys Thr Pro Arg Asn Phe Ser
 245 250 255
 Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile Phe Trp Pro
 260 265 270
 Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala Cys Cys Leu
 275 280 285
 His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser Lys Val Thr Lys Lys
 290 295 300
 Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr Gly Val Arg Gly Leu
 305 310 315 320
 His Lys Ser Leu Thr Asp Val Ala Leu Glu His His Glu Glu Cys Asp
 325 330 335
 Cys Val Cys Arg Gly Ser Thr Gly Gly
 340 345

<210> 29
 <211> 399
 <212> DNA
 <213> Orf virus

<220>
 <221> CDS
 <222> (1)..(399)

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ctg ctg aac gcg gac agc acg aaa aca tgg tcc gaa gtg ttt gaa aac 96
Leu Leu Asn Ala Asp Ser Thr Lys Thr Trp Ser Glu Val Phe Glu Asn
      20             25             30

agc ggg tgc aag cca agg ccg atg gtc ttt cga gta cac gac gag cac 144
Ser Gly Cys Lys Pro Arg Pro Met Val Phe Arg Val His Asp Glu His
      35             40             45

ccg gag cta act tct cag cgg ttc aac ccg ccg tgt gtc acg ttg atg 192
Pro Glu Leu Thr Ser Gln Arg Phe Asn Pro Pro Cys Val Thr Leu Met
      50             55             60

cga tgc ggc ggg tgc tgc aac gac gag agc tta gaa tgc gtc ccc acg 240
Arg Cys Gly Gly Cys Cys Asn Asp Glu Ser Leu Glu Cys Val Pro Thr
      65             70             75             80

gaa gag gca aac gta acg atg caa ctc atg gga gcg tcg gtc tcc ggt 288
Glu Glu Ala Asn Val Thr Met Gln Leu Met Gly Ala Ser Val Ser Gly
      85             90             95

ggg aac ggg atg caa cat ctg agc ttc gta gag cat aag aaa tgc gat 336
Gly Asn Gly Met Gln His Leu Ser Phe Val Glu His Lys Lys Cys Asp
      100            105            110

tgt aaa cca cca ctc acg acc acg cca ccg acg acc aca agg ccg ccc 384
Cys Lys Pro Pro Leu Thr Thr Thr Pro Pro Thr Thr Thr Arg Pro Pro
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aga aga cgc cgc tag 399
Arg Arg Arg Arg
      130
  
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<210> 30
 <211> 132
 <212> PRT
 <213> Orf virus

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<400> 30
Met Lys Phe Leu Val Gly Ile Leu Val Ala Val Cys Leu His Gln Tyr
  1             5             10             15

Leu Leu Asn Ala Asp Ser Thr Lys Thr Trp Ser Glu Val Phe Glu Asn
      20             25             30

Ser Gly Cys Lys Pro Arg Pro Met Val Phe Arg Val His Asp Glu His
      35             40             45
  
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Pro	Glu	Leu	Thr	Ser	Gln	Arg	Phe	Asn	Pro	Pro	Cys	Val	Thr	Leu	Met	
	50					55					60					
Arg	Cys	Gly	Gly	Cys	Cys	Asn	Asp	Glu	Ser	Leu	Glu	Cys	Val	Pro	Thr	
	65				70					75					80	
Glu	Glu	Ala	Asn	Val	Thr	Met	Gln	Leu	Met	Gly	Ala	Ser	Val	Ser	Gly	
				85					90						95	
Gly	Asn	Gly	Met	Gln	His	Leu	Ser	Phe	Val	Glu	His	Lys	Lys	Cys	Asp	
			100					105						110		
Cys	Lys	Pro	Pro	Leu	Thr	Thr	Thr	Pro	Pro	Thr	Thr	Thr	Arg	Pro	Pro	
		115					120						125			
Arg	Arg	Arg	Arg													
																130